

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (currently amended): A polypeptide isolated from a microorganism,
wherein said polypeptide has an activity to act upon a disaccharide glycoside to thereby release saccharides from said disaccharide glycoside in a disaccharide unit,
wherein said disaccharide glycoside has a glucose moiety at the aglycon side,
wherein said polypeptide has enzymatic activity at pH 2.5 to 3,
wherein said polypeptide is stable at 50°C or less,
wherein said polypeptide has an approximate molecular weight ~~in a range of about 47~~
kDa as determined by SDS-PAGE, to about 51 kDa, and
wherein said polypeptide is encoded by a nucleic acid sequence that hybridizes to the
complement of SEQ ID NO: 7 under highly stringent conditions (6X SSC, 0.1% SDS, and
68°C), and
wherein said ~~the~~ microorganism is selected from the group consisting of the genus
Aspergillus, the genus *Penicillium*, the genus *Rhizopus*, the genus *Rhizomucor*, the genus
Talaromyces, the genus *Mortierella*, the genus *Cryptococcus*, the genus *Microbacterium*, the
genus *Corynebacterium* and the genus *Actinoplanes*.

2. (currently amended): The polypeptide according to claim 1, wherein said disaccharide glycoside is selected from the group consisting of β -primeveroside, a rutinose glycoside, a gentiobiose glycoside, an arabinofuranosyl glycoside and an apiofuranosyl ~~aviofuranosyl~~ glycoside.

3. (currently amended): An isolated variant of a polypeptide having the amino acid sequence of SEQ ID NO: 8 shown in the Sequence Listing,

wherein said variant comprises an amino acid sequence having a modification of one or more amino acid residues compared with the amino acid sequence of SEQ ID NO:8, said modification selected from the group consisting of deletion, addition, insertion and substitution,

wherein said variant has at least 95% homology with the amino acid sequence of SEQ ID NO:8,

wherein said variant has an activity to act upon a disaccharide glycoside to release saccharides from said disaccharide glycoside in a disaccharide unit, wherein said disaccharide glycoside has a glucose moiety at the aglycon side,

wherein said variant has activity at pH 2.5 to 3, and

wherein said variant is stable at 50°C or less.

4. (previously presented): A polypeptide isolated from a microorganism which comprises a polypeptide having the amino acid sequence of SEQ ID NO: 8 shown in the Sequence Listing.

5-10. (canceled).

11. (currently amended): A method for producing a polypeptide having an activity to act upon a disaccharide glycoside to release saccharides from said disaccharide glycoside in a disaccharide unit, wherein said disaccharide glycoside has a glucose moiety at the aglycon side, said method comprising (1) culturing a microorganism in a nutrient medium to effect production of the polypeptide, wherein said culturing is performed under aerobic conditions with a pH in a range of 5-6, at 30°C, and wherein said nutrient medium contains a saccharide inducer, and (2) collecting said polypeptide from the resulting culture mixture,

wherein said polypeptide has enzymatic activity at pH 2.5 to 3, wherein said polypeptide is stable at 50°C or less, wherein said polypeptide has an approximate molecular weight ~~in a range of about 47 kDa as determined by SDS-PAGE, to about 51 kDa, and~~

wherein said polypeptide is encoded by a nucleic acid sequence that hybridizes to the complement of SEQ ID NO: 7 under highly stringent conditions (6X SSC, 0.1% SDS, and 68°C), and

wherein said ~~the~~ microorganism is selected from the group consisting of the genus *Aspergillus*, the genus *Penicillium*, the genus *Rhizopus*, the genus *Rhizomucor*, the genus *Talaromyces*, the genus *Mortierella*, the genus *Cryptococcus*, the genus *Microbacterium*, the genus *Corynebacterium* and the genus *Actinoplanes*.

12. (canceled).

13. (previously presented): The method for producing a polypeptide having an activity to act upon a disaccharide glycoside to release saccharides from said disaccharide glycoside in a disaccharide unit according to claim 11, wherein the polypeptide is inducible by addition of a saccharide to the nutrient medium.

14. (previously presented): The method for producing a polypeptide according to claim 13, wherein the saccharide is selected from the group consisting of gentose, gentiobiose, and gentio-oligosaccharide.

15-21. (canceled).

22. (original): An isolated polypeptide represented by amino acids 1-466 of SEQ ID NO:8.

23. (new): The isolated polypeptide of claim 1, wherein said microorganism is selected from the group consisting of the genus *Aspergillus*, the genus *Penicillium*, the genus *Rhizomucor*, and the genus *Corynebacterium*.

24. (new): The isolated polypeptide of claim 1, wherein said microorganism is selected from the group consisting of the species *Aspergillus oryzae*, *Aspergillus niger*,

Aspergillus aculeatus, *Penicillium rugulosum*, *Penicillium lilacinum*, *Penicillium decumbence*,
Penicillium multicolor, *Rhizopus oryzae*, *Rhizomucor pusillus*, *Rhizomucor miehei*, *Talaromyces*
emersonii, *Mortierella vinacea*, *Cryptococcus albidus*, *Microbacterium arborescens*,
Corynebacterium ammoniagenes, *Corynebacterium glutamicum*, and *Actinoplanes*
missouriensis.

25. (new): The method of claim 11, wherein said microorganism is selected from the group consisting of the genus *Aspergillus*, the genus *Penicillium*, the genus *Rhizomucor*, and the genus *Corynebacterium*.

26. (new): The method of claim 11, wherein said microorganism is selected from the group consisting of the species *Aspergillus oryzae*, *Aspergillus niger*, *Aspergillus aculeatus*, *Penicillium rugulosum*, *Penicillium lilacinum*, *Penicillium decumbence*, *Penicillium multicolor*, *Rhizopus oryzae*, *Rhizomucor pusillus*, *Rhizomucor miehei*, *Talaromyces emersonii*, *Mortierella vinacea*, *Cryptococcus albidus*, *Microbacterium arborescens*, *Corynebacterium ammoniagenes*, *Corynebacterium glutamicum*, and *Actinoplanes missouriensis*.